

TTATTAGGTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTGTAGATCTGTT
 1 -----+-----+-----+-----+-----+ 60
 AATAATCCAAAATGGATGGTCCTTTCGGTTGGAGCTAGAGAACATCTAGACAA

 CTCTAACGAACCTTAAAATCTGTAGCTGTCGCTGGCTGCATGCCTAGTGCACCTAC
 61 -----+-----+-----+-----+-----+ 120
 GAGATTGCTGAAATTAGACACATCGACAGCGAGCCACGTACGGATCACGTGGATG

 ...

 GTACTATGACAAATAGACAGTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAG
 15061 -----+-----+-----+-----+-----+ 15120
 CATGATACTGTTATCTGTCAAAGTAGTCTTAATAACTCAGTTATCGCGGTGATCTC

 GAGCTACTGTGTAATTGGAACAAGCAAGTTACGGTGGCTGGCATAATATGTTAAAAA
 15121 -----+-----+-----+-----+-----+ 15180
 CTCGATGACACCATTAACCTTGTGTTCAAAATGCCACCGACCGTATTATAACAATT

CANADA first PCR CA
 CTGTTACAGTGATGTAGAAACTCCACACCTTATGGGTTGGATTATCCAAAATGTGACA
 15181 -----+-----+-----+-----+-----+ 15240
 GACAAATGTCACTACATCTTGAGGTGGAATACCCAACCCTAATAGGTTTACACTGT

 GAGCCATGCCTAACATG
 GAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTGTTCTGCTCGCAAACATAACA
 15241 -----+-----+-----+-----+-----+ 15300
 CTCGGTACGGATTGTACGAATCCTATTACCGGAGAGAACAGAACGAGCGTTGTATTGT

 CTTGCTGTAACCTATCACACCGTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAA
 15301 -----+-----+-----+-----+-----+ 15360
 GAACGACATTGAATAGTGTGGCAAAGATGTCCAATCGATTGTCACACGCGTTATAATT

CANADA second PCR TGTAAACCAAGGTGGAAC
 GTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACACCAGGTGGAACATCATCCGGTG
 15361 -----+-----+-----+-----+-----+ 15420
 CACTCTACCAAGTACACACCCGCCCAGTGATATACAATTGGTCCACCTGTAGTAGGCCAC

 ATGCTACAAC TGCTTATGCTAACATTGCTTAAACATTGTCAGCTGTTACAGCCAATG
 15421 -----+-----+-----+-----+-----+ 15480
 TACGATGTTGACGAATACGATTATCACAGAAATTGTAACAGTTGACAAATGTCGGTTAC

 TAAATGCACCTCTTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTAC
 15481 -----+-----+-----+-----+-----+ 15540
 ATTACGTGAAGAAAGTTGACTACCATTATTCTATCGACTGTTCATACAGGGCGTTAGATG
 GCGTTAGATG

FIG. 1

AACACAGGCTCTATGAGTGTCTATAGAAATAGGGATGTTGATCATGAATTCTGGATG
 15541 -----+-----+-----+-----+ 15600
 TTGTGTCCGAGATACTCACAGAGATATCTTATCCCTACAACACTAGTACTTAAGCACCTAC
 TTGTGTCC CANADA second PCR

AGTTTACGCTTACCTGCGTAAACATTCTCCATGATGATTCTTCTGATGATGCCGTTG
 15601 -----+-----+-----+-----+ 15660
 TCAAAATGCGAATGGACGCATTGTAAAGAGGTAACAGAAAGACTACTACGGCAAC
 GCGAATGGACGCATTGTAA CANADA first PCR

TGTGCTATAACAGTAACATATGCGGCTCAAGGTTAGTAGCTAGCATTAAGAACCTTAAGG
 15661 -----+-----+-----+-----+ 15720
 ACACGATATTGTCATTGATACGCCGAGTTCCAATCATCGATCGTAATTCTGAAATTCC

CAGTTCTTATTATCAAAATAATGTGTTCATGTGAGGCCAAATGTTGGACTGAGACTG
 15721 -----+-----+-----+-----+ 15780
 GTCAAGAAATAATAGTTTATTACACAAGTACAGACTCCGTTACAACCTGACTCTGAC

...

GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATA
 18001 -----+-----+-----+-----+ 18060
 CATCATTCTAGTAATGACCAGAAGTAGGATGTGTCGTGGATGTGAGTCGCAACTAT

TAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAAGGCATACCAAAGGACATGACCT
 18061 -----+-----+-----+-----+ 18120
 ATTCAAGTTCTGACTCCTAATACACAACGTATGGTCCGTATGGTTCTGTACTGGA

BNIoutS2 ATGAATTACCAAGTCATGGTTAC
 ACCGTAGACTCATCTCTATGATGGGTTCAAAATGAATTACCAAGTCATGGTTACCCCTA
 18121 -----+-----+-----+-----+ 18180
 TGGCATCTGAGTAGAGACTACCCAAAGTTTACTTAATGGTCAGTTACCAATGGGAT

BNIinS GAAGCTATTGTCACGTTCG
 ATATGTTATCACCCCGAAGAAGCTATTGTCACGTTCGTGCCTGGATTGGCTTGATG
 18181 -----+-----+-----+-----+ 18240
 TATACAAATAGTGGCGCTTCTCGATAAGCAGTGCAAGCACGACCTAACCGAAACTAC

TAGAGGGCTGTCATGCAACTAGAGATGCTGTGGGTACTAACCTACCTCCAGCTAGGAT
 18241 -----+-----+-----+-----+ 18300
 ATCTCCGACAGTACGTTGATCTACGACACCCATGATTGGATGGAGAGGTCGATCCTA
 GAGGTCGATCCTA

TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACA
 18301 -----+-----+-----+-----+ 18360
 AAAGATGTCCACAATTGAATCATCGACATGGCTGACCAATAACTGTGACTTTATTGT
 AAAGATGTC BNIinAS
 CATCGACATGGCTGACCAATAC BNIoutAS

FIG. 1 cont.

CAGAATTCAACCAGAGTTAATGCAAACCTCCACCAGGTGACCAGTTAACATCTTATAC
 18361 -----+-----+-----+-----+-----+ 18420
 GTCTTAAGTGGTCTCAATTACGTTGGAGGTGGTCCACTGGTCAAATTGTAGAATATG

CACTCATGTATAAAGGCTGCCCTGGAATGTAGTGCCTTAAGATAGTACAAATGCTCA
 18421 -----+-----+-----+-----+-----+ 18480
 GTGAGTACATATTCCGAACGGGACCTTACATCACGCATAATTCTATCATGTTACGAGT

...

TACCGAAGAGCTACCCGACGAGTCGTGGTGGTGACGGAAAATGAAAGAGCTCAGCCCC
 28381 -----+-----+-----+-----+-----+ 28440
 ATGGCTCTCGATGGGCTGCTCAAGCACCACACTGCCGTTTACTTCTCGAGTCGGGG

AGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCTTCACTTCCCTACGGCGCTAAC
 28441 -----+-----+-----+-----+-----+ 28500
 TCTACCATGAAGATAATGGATCCTGACC GGCTTCAAGTGAAGGGATGCCGCGATTG

CIID-28506F AGGCATCGTATGGGTGCA

C IID-28529T AGGGAGCCTTGAATACACCCAAAGACCA

AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTGAATAACACCCAAAGACCA CATT
 28501 -----+-----+-----+-----+-----+ 28560
 TTTCTTCCGTAGCATACCCAACGTTGACTCCCTCGGAACCTATGTGGGTTCTGGTGTAA

GGCACCCGCAATCTAATAACAATGCTGCCACCGTGCTACAACCTCCTCAAGGAACAACA
 28561 -----+-----+-----+-----+-----+ 28620
 CCGTGGGCGTTAGGATTATTGTTACGACGGTGGCACGATGTTGAAGGGAGTCCTTGTGTTGT

TTGCCAAAAGGCTTACGCAGAGGGAAAGCAGAGGCGGCAGTCAAGCCTTCTCGCTCC
 28621 -----+-----+-----+-----+-----+ 28680
 AACGGTTTCCGAAGATGCGTCTCCCTCGTCTCCGCCGTCAAGTCGGAGAACAGCGAGG
 AACGGTTTCCGAAG C IID-28614R

TCATCACGTAGTCGGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCT
 28681 -----+-----+-----+-----+-----+ 28740
 AGTAGTGCATCAGGCCATTAAAGTTCTTAAGTTGAGGACCGTCGTCACTCCCTTAAGA

CCTGCTCGAATGGCTAGCGGAGGTGGTGAAGACTGCCCTCGCGCTATTGCTGCTAGACAGA
 28741 -----+-----+-----+-----+-----+ 28800
 GGACGAGCTTACCGATCGCCTCCACCACTTGACGGGAGCGCGATAACGACGATCTGTCT

TTGAACCAGCTTGAGAGCAAAGTTCTGGTAAAGGCCAACACAACAAGGCCAAACTGTC
 28801 -----+-----+-----+-----+-----+ 28860
 AACTTGGTCGAACTCTCGTTCAAAGACCATTCCGGTTGTTGTTCCGGTTGACAG

C IID-28891F AAGCCTCGCCAAAAACGTAC

ACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTGCCAAAAACGTACTGCCACAAAA
 28861 -----+-----+-----+-----+-----+ 28920
 TGATTCTTAGACGACGACTCCGTAGATTTCGGAGCGGGTTTGCATGACGGTGTGTT

FIG. 1 cont.

CAGTACAACGTCACTCAAGCATTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTTC
 28921 -----+-----+-----+-----+-----+ 28980
 GTCATGTTGCAGTGAGTCGAAACCCCTCTGCACCAGGTCTGTTGGGTCCTTAAAG

GGGGACCAAGACCTAATCAGACAAGGAACGTACAAACATTGCCGCAAATTGCACAA
 28981 -----+-----+-----+-----+-----+ 29040
 CCCCTGGTTCTGGATTAGTCTGTTCCITGACTAATGTTGTAACCGGCGTTAACGTGTT

CIID-29074T TCACGCATTGGCATGGAAGTCACAC
 TTTGCTCCAAGTGCCTCTGCATTCTTGAATGTCACGCATTGGCATGGAAGTCACACCT
 29041 -----+-----+-----+-----+-----+ 29100
 AAACGAGGTTACGGAGACGTAAGAAACCTACAGTGCCTAACCGTACCTCAGTGTGGA
 A

TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATT
 29101 -----+-----+-----+-----+-----+ 29160
 AGCCCTTGTACCGACTGAATAGTACCTCGGTAACTAACCTACTGTTCTAGGTGTTAAG
 AGCCCTTGTACCGACTGAA CIID-29100R

AAAGACAACGTCTACTGCTGAACAAGCACATTGACGCATAAAAACATTCCCACCAACA
 29161 -----+-----+-----+-----+-----+ 29220
 TTTCTGTTGCAGTATGACGACTTGTCTGTAACTGCGTATGTTGTAAGGGTGGTTGT

GAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTGCCGCAGAGACAA
 29221 -----+-----+-----+-----+-----+ 29280
 CTCGGATTTTCTGTTCTTCTGACTACTCGAGTCGGAAACGGCGTCTCTGTT

AAGAAGCAGCCCAGTGTGACTCTTCTTGTGCGGCTGACATGGATGATTCTCCAGACAA
 29281 -----+-----+-----+-----+-----+ 29340
 TTCTCGTCGGGTGACACTGAGAAGAAGGACGCCACTGTACCTACTAAAGAGGTCTGTT

CIID-29398F ATG
 CTTCAAAATCCATGAGTGGAGCTCTGCTGATTCAACTCAGGCATAAACACTCATGATG
 29341 -----+-----+-----+-----+-----+ 29400
 GAAGTTTAAGGTACTCACCTCGAAGACGACTAAGTTGAGTCCGTATTGTGAGTACTAC

CIID-29426F AAACGTTTCGCAATTCCGT
CIID-29405F CACAAGGCAGATGGCTATGT
 ACCACACAAGGCACATGG
 ACCACACAAGGCAGATGGCTATGTAAACGTTTCGCAATTCCGTTACGATACATAGTC
 29401 -----+-----+-----+-----+-----+ 29460
 TGGTGTGTTCCGTCTACCGATACATTGCAAAAGCGTTAAGGCAAATGCTATGTATCAG

TACTCTGTGAGAATGAATTCTCGTAACAAACAGCACAAGTAGGTTAGTTAACTTTA
 29461 -----+-----+-----+-----+-----+ 29520
 ATGAGAACACGTCTACTTAAGAGCATTGATTGTCGTGTTACATCCAAATCAATTGAAAT

ATCTCACATAGCAATTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGGCCACCA
 29521 -----+-----+-----+-----+-----+ 29580
 TAGAGTGTATCGTTAGAAATTAGTTACACATTGTAATCCCTCCTGAACCTTCTCGGTGGT

FIG. 1 cont.

CIID-29584T TTTCATCGAGGCCACGCGGAGTAC
CATTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAG
29581 -----+-----+-----+-----+-----+ 29640
GTAAAAGTAGCTCCGGTGCGCCTCATGCTAGCTCCCATGTCACTTATTACGATCCCTCTC
TGTCACTTATTGCGATCCCTCTC
GTCACCTATTGCGATCCCTCTC
TGTCACTTATTACGATCCCTCTC
CTTATTACGATCCCTCTC
TCCGGTGCGCCTCATGCTAGCT CIID-29592T

CTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAAATTAGTAGTGCTATCCCCATGTG
29641 -----+-----+-----+-----+-----+ 29700
GACGGATATACCTTCTCGGGATTACACATTTAATTAAAATCATCACGATAGGGTACAC
G 29618R
G 29619R
G 29618-2R
GACGG CIID-29623R

ATTTTAATAGCTTCTTAGGAGAATGAC
29701 -----+-----+----- 29727
TAAAATTATCGAAGAACCTCTTACTG

FIG. 1 cont.

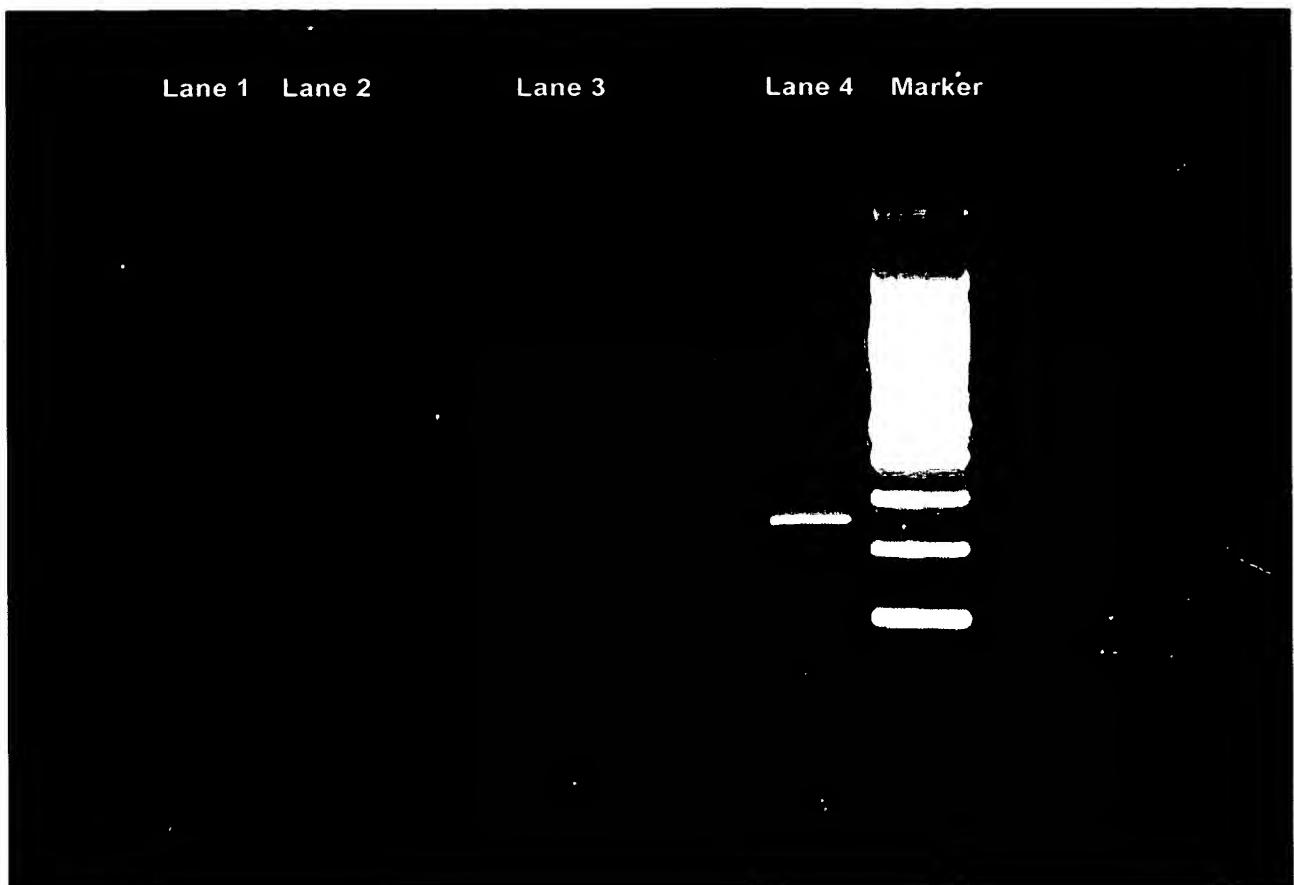


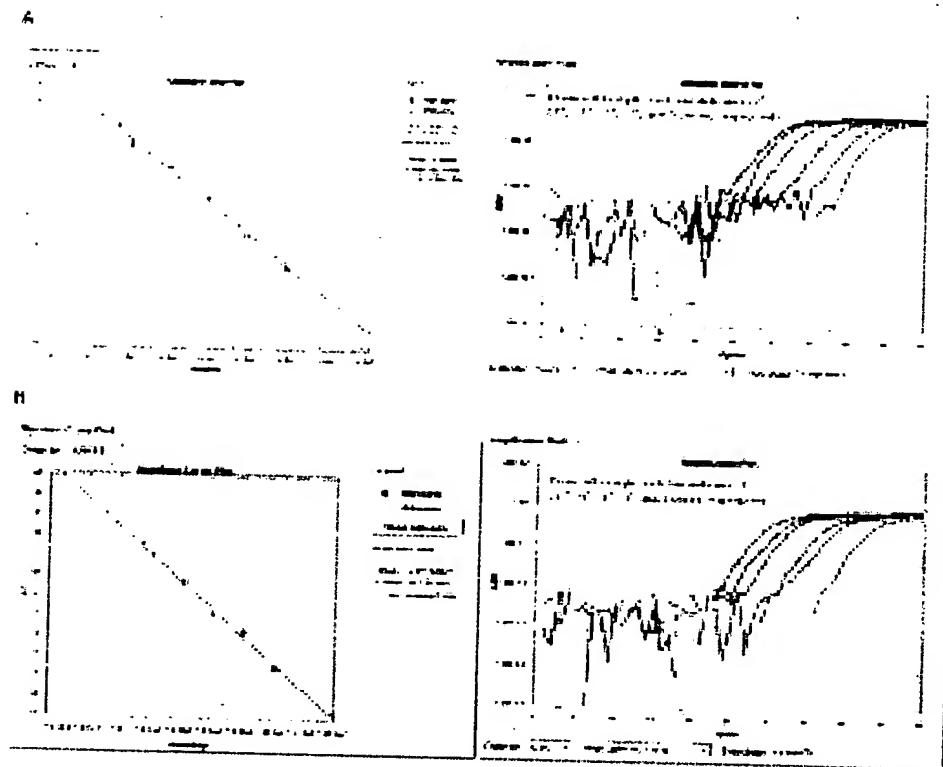
FIG. 2

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AGGCATCGTATGGGTTGCAACTGAGGGAGCCTGAATAACACCCAAAGACCACATTGGCACCCGCA
ATCCTAATAACAATGCTGCCACCGTGCTACAACCTCTCAAGGAACAACATTGCCAAAAGGCTTCT
ACGCAGAGGAAGCAGAGCGGGCACTCAAGCCTCTTCGCTCTCATCACGTAGTCGCGGTAAAT
TCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCTGCTCGAATGGCTAGCGGAGGTGG
TGAAACTGCCCTCGCGTATTGCTGCTAGACAGATTGAACCAGCTTGAGAGCAGAAAGTTCTGGTAA
AGGCCAACAAACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTC
GCCAAAAACGTACTGCCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAA
CAAACCCAAGGAAATTGGGGACCAAGACCTAATCAGACAAGGAACGTGATTACAAACATTGGCC
GCAAATTGCAACAATTGCTCCAAGTGCCTCTGCATTCTTGGAAATGTCACCGCATTGGCATGGAAGT
CACACCTTCGGAACATGGTGACTIONTATCATGGAGCCATTAATTGGATGACAAAGATCCACAATT
CAAAGACAAACGTCAACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGAGC
CTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTGGCGCAGAGACAAAAGAAGCA
GCCCACTGTGACTCTTCTTCGCGGCTGACATGGATGATTCTCCAGACAACCTCAAAATTCCATG
AGTGGAGCTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCACACAAGGCAGATGGC
TATGTAAACGTTTCGCAATTCCGTTACGATACATAGTCTACTCTTGTGCAGAATGAATTCTCGTA
ACTAAACAGCACAAGTAGGTTAGTTAATTCACTCACATAGCAATCTTAATCAATGTGAAC
ATTAGGGAGGACTTGAAAGAGCCACACATTTCATCGAGGCCACGCCAGTACGATCGAGGGTA
CAGTGAATAATGCTAGGGAGAGC

FIG. 3

FIG. 4



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FIG. 5A

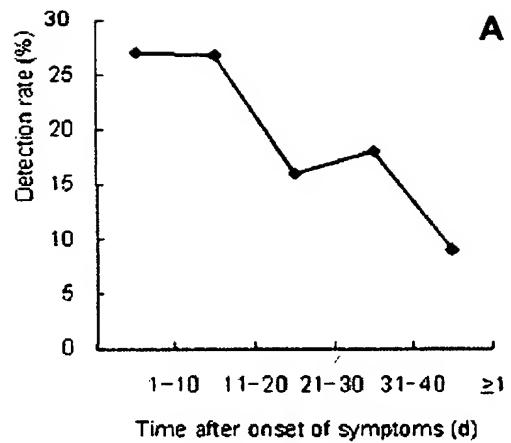


FIG. 5B

